

Database : GenEmbl:*
 1: gb_ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | Query Match | Length | DB | ID | Description |
|--------|-----|-------|-------------|--------|----|-------------|--------------------|
| | 1 | 834 | 59.1 | 834 | 6 | BD141394 | BD141394 Novel car |
| | 2 | 437.4 | 31.0 | 110000 | 1 | AP006840_07 | Continuation (8 of |
| | 3 | 372.4 | 26.4 | 341887 | 1 | AP003006 | AP003006 Mesorhizo |
| c | 4 | 366 | 26.0 | 299425 | 1 | AP005049 | AP005049 Streptomy |
| | 5 | 344.8 | 24.5 | 294800 | 1 | SME591789 | AL591789 Sinorhizo |
| | 6 | 340.4 | 24.1 | 110000 | 1 | BX571965_10 | Continuation (11 o |
| | 7 | 339.8 | 24.1 | 10386 | 1 | AE004515 | AE004515 Pseudomon |
| c | 8 | 338.8 | 24.0 | 110000 | 1 | CP000010_23 | Continuation (24 o |
| | 9 | 335.8 | 23.8 | 822 | 12 | AY658815 | AY658815 Synthetic |
| | 10 | 317.2 | 22.5 | 310967 | 1 | AE016869 | AE016869 Pseudomon |
| c | 11 | 315.6 | 22.4 | 300395 | 1 | AE016785 | AE016785 Pseudomon |
| | 12 | 310.8 | 22.0 | 1084 | 6 | AX477714 | AX477714 Sequence |
| | 13 | 293.8 | 20.8 | 10325 | 1 | AE009154 | AE009154 Agrobacte |

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | % | | Query | | DB | ID | Description |
|---------------|-------|-------|--------|---|----------|----------|-------------|
| | Score | Match | Length | | | | |
| 1 | 1455 | 100.0 | 277 | 5 | AAO16951 | Aao16951 | M luteus |
| 2 | 871 | 59.9 | 281 | 8 | ADS23099 | Ads23099 | Bacterial |
| 3 | 812 | 55.8 | 352 | 7 | ABO80918 | Abo80918 | Pseudomon |
| 4 | 810 | 55.7 | 277 | 8 | ADS22524 | Ads22524 | Bacterial |
| 5 | 806 | 55.4 | 281 | 6 | ABU22187 | Abu22187 | Protein e |
| 6 | 783 | 53.8 | 266 | 8 | ADS25492 | Ads25492 | Bacterial |
| 7 | 783 | 53.8 | 266 | 8 | ADS25964 | Ads25964 | Bacterial |
| 8 | 783 | 53.8 | 266 | 8 | ADS25281 | Ads25281 | Bacterial |
| 9 | 777 | 53.4 | 276 | 8 | ADN25959 | Adn25959 | Bacterial |
| 10 | 774 | 53.2 | 273 | 8 | ADS25018 | Ads25018 | Bacterial |
| 11 | 772 | 53.1 | 281 | 6 | ABU21692 | Abu21692 | Protein e |
| 12 | 765 | 52.6 | 273 | 5 | AAE25028 | Aae25028 | Human dru |
| 13 | 752 | 51.7 | 284 | 8 | ADN18215 | Adn18215 | Bacterial |
| 14 | 749 | 51.5 | 273 | 6 | ABU41426 | Abu41426 | Protein e |
| 15 | 706 | 48.5 | 256 | 8 | ADN24621 | Adn24621 | Bacterial |
| 16 | 706 | 48.5 | 256 | 8 | ADN21862 | Adn21862 | Bacterial |
| 17 | 686.5 | 47.2 | 324 | 7 | ABO61379 | Abo61379 | Klebsiell |
| 18 | 682.5 | 46.9 | 265 | 8 | ADS30915 | Ads30915 | Bacterial |
| 19 | 656 | 45.1 | 275 | 8 | ADS30423 | Ads30423 | Bacterial |

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|----------|--------------------|
| | | Match | Length | | | |
| 1 | 1410 | 100.0 | 1410 | 6 | AAL45070 | Aal45070 M luteus |
| 2 | 834 | 59.1 | 834 | 6 | AAL45071 | Aal45071 M luteus |
| 3 | 370.8 | 26.3 | 846 | 13 | ADS60145 | Ads60145 Bacterial |
| 4 | 347.8 | 24.7 | 843 | 8 | ACA25562 | Aca25562 Prokaryot |
| 5 | 346.2 | 24.6 | 1059 | 11 | ABD14489 | Abd14489 Pseudomon |
| 6 | 334.8 | 23.7 | 843 | 8 | ACA26057 | Aca26057 Prokaryot |
| 7 | 333.8 | 23.7 | 828 | 13 | ADS56625 | Ads56625 Bacterial |
| 8 | 324.4 | 23.0 | 768 | 13 | ADS49772 | Ads49772 Bacterial |
| 9 | 324.4 | 23.0 | 768 | 13 | ADS55287 | Ads55287 Bacterial |
| 10 | 316.8 | 22.5 | 819 | 13 | ADS62064 | Ads62064 Bacterial |
| 11 | 314.2 | 22.3 | 819 | 8 | ACA45296 | Aca45296 Prokaryot |
| 12 | 310.8 | 22.0 | 1084 | 6 | AAD40577 | Aad40577 Human dru |
| 13 | 290.4 | 20.6 | 831 | 13 | ADS59570 | Ads59570 Bacterial |
| 14 | 285.6 | 20.3 | 798 | 13 | ADS63010 | Ads63010 Bacterial |
| 15 | 285.6 | 20.3 | 798 | 13 | ADS62327 | Ads62327 Bacterial |
| 16 | 285.6 | 20.3 | 798 | 13 | ADS62538 | Ads62538 B |

Title: US-10-088-920A-2
 Perfect score: 1410
 Sequence: 1 ggtacccgcccgcctcctat.....tcgaggaaggaacggagctc 1410

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | % | | | | | | Description |
|--------|-----|-------|-------------|---------|----|----------------------|-------------------|
| | No. | Score | Query Match | Length | DB | ID | |
| | 1 | 346.2 | 24.6 | 1059 | 4 | US-09-252-991A-13093 | Sequence 13093, A |
| | 2 | 288 | 20.4 | 21330 | 4 | US-09-902-540-1209 | Sequence 1209, Ap |
| c | 3 | 282.6 | 20.0 | 681 | 4 | US-09-252-991A-12847 | Sequence 12847, A |
| | 4 | 281.4 | 20.0 | 819 | 4 | US-09-902-540-4212 | Sequence 4212, Ap |
| | 5 | 226.2 | 16.0 | 975 | 4 | US-09-489-039A-725 | Sequence 725, App |
| c | 6 | 217 | 15.4 | 564 | 4 | US-09-252-991A-12700 | Sequence 12700, A |
| c | 7 | 154.2 | 10.9 | 438 | 4 | US-09-489-039A-666 | Sequence 666, App |
| c | 8 | 92.4 | 6.6 | 2031 | 4 | US-09-634-238-129 | Sequence 129, App |
| | 9 | 82 | 5.8 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appli |
| | 10 | 82 | 5.8 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appli |
| | 11 | 81 | 5.7 | 1077 | 4 | US-09-252-991A-14964 | Sequence 14964, A |

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

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SUMMARIES

| Result | % | | Query | | | | Description |
|--------|-----|-------|-------|---------|----|----------------------|-------------------|
| | No. | Score | Match | Length | DB | ID | |
| c | 1 | 1410 | 100.0 | 1410 | 16 | US-10-088-920A-2 | Sequence 2, Appli |
| | 2 | 370.8 | 26.3 | 846 | 17 | US-10-369-493-35819 | Sequence 35819, A |
| | 3 | 366 | 26.0 | 9025608 | 15 | US-10-156-761-1 | Sequence 1, Appli |
| | 4 | 363.6 | 25.8 | 843 | 15 | US-10-156-761-7212 | Sequence 7212, Ap |
| | 5 | 347.8 | 24.7 | 843 | 17 | US-10-282-122A-13432 | Sequence 13432, A |
| | 6 | 334.8 | 23.7 | 843 | 17 | US-10-282-122A-13927 | Sequence 13927, A |
| | 7 | 333.8 | 23.7 | 828 | 17 | US-10-369-493-32299 | Sequence 32299, A |
| | 8 | 324.4 | 23.0 | 768 | 17 | US-10-369-493-28202 | Sequence 28202, A |
| | 9 | 324.4 | 23.0 | 768 | 17 | US-10-369-493-30961 | Sequence 30961, A |

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_htc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | % | | | | | | | |
|--------|-------|-------|--------|------|----|----------|--|-------------|-----------|
| Result | | Query | | | | | | | |
| No. | Score | Match | Length | DB | ID | | | Description | |
| c | 1 | 169.6 | 12.0 | 929 | 8 | BZ570067 | | BZ570067 | msh2_115. |
| | 2 | 120.8 | 8.6 | 608 | 9 | CG913045 | | CG913045 | ZMMBBb037 |
| c | 3 | 119.6 | 8.5 | 812 | 9 | BX908536 | | BX908536 | Leishmani |
| c | 4 | 80.2 | 5.7 | 1516 | 4 | BG809984 | | BG809984 | mgct002xd |
| | 5 | 79.2 | 5.6 | 458 | 8 | AQ868055 | | AQ868055 | nbeb0017D |
| | 6 | 78.6 | 5.6 | 1516 | 4 | BG809984 | | BG809984 | mgct002xd |
| | 7 | 78.4 | 5.6 | 1821 | 9 | CL090560 | | CL090560 | ISB1-17N1 |
| c | 8 | 76.2 | 5.4 | 1780 | 9 | AG448243 | | AG448243 | Mus muscu |
| c | 9 | 76 | 5.4 | 1131 | 9 | AG042920 | | AG042920 | Pan trogl |
| | 10 | 75 | 5.3 | 457 | 8 | BZ895098 | | BZ895098 | Hg7_0124 |
| | 11 | 73.8 | 5.2 | 1780 | 9 | AG448243 | | AG448243 | Mus muscu |
| c | 12 | 73.2 | 5.2 | 1798 | 9 | AG171124 | | AG171124 | Pan trogl |
| | 13 | 73 | 5.2 | 925 | 9 | CNS0091P | | AL053013 | Drosophil |
| c | 14 | 72.8 | 5.2 | 925 | 9 | CNS0091P | | AL053013 | Drosophil |
| | 15 | 72 | 5.1 | 462 | 5 | BQ640772 | | BQ640772 | TVEST004. |
| | 16 | 71.2 | 5.0 | 984 | 8 | BZ560840 | | BZ560840 | pacs2-164 |
| | 17 | 70.2 | 5.0 | 2483 | 9 | CL496067 | | CL496067 | SAIL_619_ |
| c | 18 | 69.8 | 5.0 | 1821 | 9 | CL090560 | | CL090560 | ISB1-17N1 |
| | 19 | 69.6 | 4.9 | 2243 | 9 | AG381986 | | AG381986 | Mus muscu |

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | % Query | | Length | DB | ID | Description |
|---------------|------------|-------|--------|----|----------------------|-------------------|
| | Score | Match | | | | |
| 1 | 812 | 55.8 | 352 | 4 | US-09-252-991A-29664 | Sequence 29664, A |
| 2 | 686.5 | 47.2 | 324 | 4 | US-09-489-039A-7896 | Sequence 7896, Ap |
| 3 | 568 | 39.0 | 240 | 4 | US-09-902-540-11508 | Sequence 11508, A |
| 4 | 346.5 | 23.8 | 358 | 4 | US-09-252-991A-31535 | Sequence 31535, A |
| 5 | 337 | 23.2 | 306 | 4 | US-09-902-540-9859 | Sequence 9859, Ap |
| 6 | 329.5 | 22.6 | 350 | 4 | US-09-489-039A-9552 | Sequence 9552, Ap |
| 7 | 318.5 | 21.9 | 328 | 4 | US-09-489-039A-12803 | Sequence 12803, A |
| 8 | 308.5 | 21.2 | 292 | 4 | US-09-489-039A-12672 | Sequence 12672, A |
| 9 | 307 | 21.1 | 291 | 4 | US-09-107-532A-5063 | Sequence 5063, Ap |
| 10 | 300 | 20.6 | 314 | 4 | US-09-902-540-14628 | Sequence 14628, A |
| 11 | 298.5 | 20.5 | 330 | 4 | US-09-724-797-28 | Sequence 28, Appl |
| 12 | 297.5 | 20.4 | 332 | 4 | US-09-107-532A-6891 | Sequence 6891, Ap |
| 13 | 297 | 20.4 | 243 | 4 | US-09-134-000C-6794 | Sequence 6794, Ap |
| 14 | 294.5 | 20.2 | 321 | 4 | US-09-489-039A-13361 | Sequence 13361, A |
| 15 | 291.5 | 20.0 | 348 | 4 | US-09-673-198-4 | Sequence 4, Appli |
| 16 | 291 | 20.0 | 298 | 4 | US-09-134-000C-6059 | Sequence 6059, Ap |
| 17 | 288.5 | 19.8 | 316 | 1 | US-08-585-595-3 | Sequence 3, Appli |
| 18 | 288 | 19.8 | 330 | 4 | US-09-679-279-10 | Sequence 10, Appl |
| 19 | 288 | 19.8 | 351 | 4 | US-09-489-039A-11976 | Sequence 11976, A |
| 20 | 287.5 | 19.8 | 351 | 4 | US-09-252-991A-19370 | Sequence 19370, A |
| 21 | 284.5 | 19.6 | 316 | 3 | US-08-801-344-4 | Sequence 4, Appli |
| 22 | 284.5 | 19.6 | 316 | 3 | US-09-498-599-4 | Sequence 4, Appli |
| 23 | 283.5 | 19.5 | 279 | 4 | US-09-543-681A-7803 | Sequence 7803, Ap |
| 24 | 280 | 19.2 | 341 | 4 | US-09-252-991A-30076 | Sequence 30076, A |
| 25 | 279.5 | 19.2 | 334 | 4 | US-09-328-352-6079 | Sequence 6079, Ap |
| 26 | 276.5 | 19.0 | 290 | 4 | US-09-248-796A-17316 | Sequence 17316, A |

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | Length | DB | ID | Description |
|---------------|-------|------------|--|--------|----|----------------------|--------------------|
| | | Match | | | | | |
| 1 | 1455 | 100.0 | | 277 | 14 | US-10-088-920A-1 | Sequence 1, Appli |
| 2 | 881.5 | 60.6 | | 281 | 14 | US-10-156-761-14762 | Sequence 14762, A |
| 3 | 871 | 59.9 | | 281 | 15 | US-10-369-493-12132 | Sequence 12132, A |
| 4 | 810 | 55.7 | | 277 | 15 | US-10-369-493-11557 | Sequence 11557, A |
| 5 | 806 | 55.4 | | 281 | 15 | US-10-282-122A-50111 | Sequence 50111, A |
| 6 | 783 | 53.8 | | 266 | 15 | US-10-369-493-14314 | Sequence 14314, A |
| 7 | 783 | 53.8 | | 266 | 15 | US-10-369-493-14525 | Sequence 14525, A |
| 8 | 783 | 53.8 | | 266 | 15 | US-10-369-493-14997 | Sequence 14997, A |
| 9 | 777 | 53.4 | | 276 | 15 | US-10-369-493-8612 | Sequence 8612, Ap. |
| 10 | 774 | 53.2 | | 273 | 15 | US-10-369-493-14051 | Sequence 14051, A |

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|--------|--------------------|
| | | Match | Length | | | |
| 1 | 810 | 55.7 | 281 | 2 | A97604 | probable oxidoredu |
| 2 | 810 | 55.7 | 281 | 2 | AB2826 | aldo/keto reductas |
| 3 | 803 | 55.2 | 273 | 2 | A83546 | probable oxidoredu |
| 4 | 752 | 51.7 | 284 | 1 | E64938 | probable aldehyde |
| 5 | 749 | 51.5 | 284 | 2 | F85788 | probable an aldehy |
| 6 | 749 | 51.5 | 284 | 2 | B90940 | probable an aldehy |
| 7 | 723.5 | 49.7 | 285 | 2 | AI0711 | probable oxidoredu |
| 8 | 486 | 33.4 | 274 | 2 | F72218 | oxidoreductase, al |
| 9 | 448.5 | 30.8 | 273 | 2 | D71221 | probable morphine |
| 10 | 441.5 | 30.3 | 279 | 2 | F75188 | morphine 6-dehydro |
| 11 | 416 | 28.6 | 292 | 2 | B90454 | dehydrogenase [imp |
| 12 | 400 | 27.5 | 319 | 2 | AH2062 | aldo/keto reductas |
| 13 | 396.5 | 27.3 | 265 | 2 | B90506 | oxidoreductase, al |
| 14 | 375.5 | 25.8 | 277 | 2 | B84205 | aldehyde reductase |
| 15 | 362.5 | 24.9 | 354 | 2 | T44934 | mocA protein [impo |
| 16 | 351 | 24.1 | 304 | 2 | H90466 | oxidoreductase [im |
| 17 | 346.5 | 23.8 | 331 | 2 | H83328 | probable oxidoredu |
| 18 | 345.5 | 23.7 | 294 | 2 | AC3642 | 2,5-diketo-D-gluc |
| 19 | 344.5 | 23.7 | 348 | 2 | AB3121 | oxidoreductase moc |
| 20 | 344.5 | 23.7 | 395 | 2 | E98166 | mocA protein [impo |
| 21 | 344 | 23.6 | 331 | 2 | B95902 | probable aldoketo |
| 22 | 340.5 | 23.4 | 276 | 2 | C70040 | plant-metabolite d |
| 23 | 340 | 23.4 | 276 | 2 | F83919 | plant-metabolite d |
| 24 | 335 | 23.0 | 278 | 2 | A84131 | plant-metabolite d |
| 25 | 332 | 22.8 | 329 | 2 | AG0519 | probable aldo/keto |
| 26 | 324.5 | 22.3 | 314 | 2 | S75995 | hypothetical prote |
| 27 | 324 | 22.3 | 280 | 2 | D69988 | plant metabolite d |
| 28 | 324 | 22.3 | 332 | 2 | D98252 | general stress pro |

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|------------|--------------------|
| 1 | 957 | 65.8 | 280 | 2 | Q67RQ0 | Q67rq0 symbiobacte |
| 2 | 881.5 | 60.6 | 281 | 2 | Q826G0 | Q826g0 streptomyce |
| 3 | 871 | 59.9 | 281 | 2 | Q98C22 | Q98c22 rhizobium l |
| 4 | 810 | 55.7 | 281 | 2 | Q8UDT7 | Q8udt7 agrobacteri |
| 5 | 807 | 55.5 | 281 | 2 | Q63WJ9 | Q63wj9 burkholderi |
| 6 | 806 | 55.4 | 281 | 2 | Q62HK0 | Q62hk0 burkholderi |
| 7 | 805 | 55.3 | 281 | 2 | Q92NR7 | Q92nr7 rhizobium m |
| 8 | 803 | 55.2 | 273 | 2 | Q9I5D4 | Q9i5d4 pseudomonas |
| 9 | 754 | 51.8 | 299 | 2 | Q8FGW6 | Q8fgw6 escherichia |
| 10 | 752 | 51.7 | 284 | 1 | YEAE_ECOLI | P76234 escherichia |
| 11 | 749 | 51.5 | 273 | 2 | Q87YU2 | Q87yu2 pseudomonas |
| 12 | 749 | 51.5 | 284 | 2 | Q8XDT9 | Q8xdt9 escherichia |
| 13 | 742.5 | 51.0 | 253 | 2 | Q88I81 | Q88i81 pseudomonas |
| 14 | 725.5 | 49.9 | 283 | 2 | Q6D4P4 | Q6d4p4 erwinia car |
| 15 | 724.5 | 49.8 | 285 | 2 | Q8ZPW0 | Q8zpw0 salmonella |
| 16 | 723.5 | 49.7 | 285 | 2 | Q8Z6F0 | Q8z6f0 salmonella |
| 17 | 671.5 | 46.2 | 286 | 2 | Q89RG2 | Q89rg2 bradyrhizob |
| 18 | 663.5 | 45.6 | 253 | 2 | Q7UCK6 | Q7uck6 shigella fl |
| 19 | 662.5 | 45.5 | 253 | 2 | Q83RH8 | Q83rh8 shigella fl |
| 20 | 658.5 | 45.3 | 277 | 2 | Q6N7V4 | Q6n7v4 rhodopseudo |
| 21 | 635.5 | 43.7 | 284 | 2 | Q8PBK9 | Q8pbk9 xanthomonas |
| 22 | 630.5 | 43.3 | 281 | 2 | Q7WAQ1 | Q7waq1 bordetella |
| 23 | 630.5 | 43.3 | 284 | 2 | Q8PN61 | Q8pn61 xanthomonas |
| 24 | 623.5 | 42.9 | 281 | 2 | Q7WJV6 | Q7wjv6 bordetella |
| 25 | 597 | 41.0 | 279 | 2 | Q74HC5 | Q74hc5 lactobacill |
| 26 | 532 | 36.6 | 256 | 2 | Q9Z657 | Q9z657 zymomonas m |
| 27 | 525 | 36.1 | 283 | 2 | Q65UR6 | Q65ur6 mannheimia |